

SEQUENCE LISTING

<110> Rosanne M. Crooke
Mark J. Graham

<120> ANTISENSE MODULATION OF MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN
EXPRESSION

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<223> Antisense Oligonucleotide

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<213> Homo sapiens

<220>

<221> CDS

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Met Ile Leu Leu Ala Val Leu Phe Leu

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Cys Phe Ile Ser Ser Tyr Ser Ala Ser Val Lys Gly His Thr Thr Gly
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ctc tca tta aat aat gac cgg ctg tac aag ctc acg tac tcc act gaa	209
Leu Ser Leu Asn Asn Asp Arg Leu Tyr Lys Leu Thr Tyr Ser Thr Glu	
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Val Leu Leu Asp Arg Gly Lys Gly Lys Leu Gln Asp Ser Val Gly Tyr	
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Arg Ile Ser Ser Asn Val Asp Val Ala Leu Leu Trp Arg Asn Pro Asp	
60 65 70	
ggg gat gat gac cag ttg atc caa ata acg atg aag gat gta aat gtt	353
Gly Asp Asp Asp Gln Leu Ile Gln Ile Thr Met Lys Asp Val Asn Val	
75 80 85	
gaa aat gtg aat cag cag aga gga gag aag agc atc ttc aaa gga aaa	401
Glu Asn Val Asn Gln Gln Arg Gly Glu Lys Ser Ile Phe Lys Gly Lys	
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Ser Pro Ser Ser Lys Ile Met Gly Lys Glu Asn Leu Glu Ala Leu Gln Arg	
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Pro Thr Leu Leu His Leu Ile His Gly Lys Val Lys Glu Phe Tyr Ser	
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Tyr Gln Asn Glu Ala Val Ala Ile Glu Asn Ile Lys Arg Gly Leu Ala	
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Ser Leu Phe Gln Thr Gln Leu Ser Ser Gly Thr Thr Asn Glu Val Asp	
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Ile Ser Gly Asn Cys Lys Val Thr Tyr Gln Ala His Gln Asp Lys Val	
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Ile Lys Ile Lys Ala Leu Asp Ser Cys Lys Ile Ala Arg Ser Gly Phe	
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Thr Thr Tyr Lys Ile Glu Asp Ser Phe Val Ile Ala Val Leu Ala Glu	
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Glu Thr His Asn Phe Gly Leu Asn Phe Leu Gln Thr Ile Lys Gly Lys	
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Arg	Leu	Met	Ser	Gly	Lys	Gln	Ala	Ala	Ala	Ile	Ile	Lys	Ala	Val	Asp	
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tca	aag	tac	acg	gcc	att	ccc	att	gtg	ggg	cag	gtc	ttc	cag	agc	cac	977
Ser	Lys	Tyr	Thr	Ala	Ile	Pro	Ile	Val	Gly	Gln	Val	Phe	Gln	Ser	His	
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Cys	Lys	Gly	Cys	Pro	Ser	Leu	Ser	Glu	Leu	Trp	Arg	Ser	Thr	Arg	Lys	
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Tyr	Leu	Gln	Pro	Asp	Asn	Leu	Ser	Lys	Ala	Glu	Ala	Val	Arg	Asn	Phe	
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Gln	Ile	Leu	Lys	Met	Glu	Asn	Lys	Glu	Val	Leu	Pro	Gln	Leu	Val	Asp	
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Phe	Leu	Asp	Phe	Lys	Ser	Asp	Ser	Ser	Ile	Ile	Leu	Gln	Glu	Arg	Phe	
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gcc	ctc	att	agt	aag	ttc	aaa	ggg	tct	att	ggg	agc	agt	gac	atc	aga	1361
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gat	gtt	cag	ctc	aga	cct	gtc	acc	ttt	ttc	aac	gga	tac	agt	gat	ttg	2225		
Asp	Val	Gln	Leu	Arg	Pro	Val	Thr	Phe	Phe	Asn	Gly	Tyr	Ser	Asp	Leu</			

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Ser Leu Phe Gln Met Gln Leu Ser Ser Gly Thr Thr Asn Glu Val Asp	
155 160 165	
atc tct ggg gat tgt aaa gtg acc tac cag gcc caa caa gac aaa gtg	579
Ile Ser Gly Asp Cys Lys Val Thr Tyr Gln Ala Gln Gln Asp Lys Val	
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Val Lys Ile Lys Ala Leu Asp Thr Cys Lys Ile Glu Arg Ser Gly Phe	
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Thr Thr Ala Asn Gln Val Leu Gly Val Ser Ser Lys Ala Thr Ser Val	
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Glu Thr Arg Ala Phe Ala Leu Asn Phe Gln Gln Thr Ile Ala Gly Lys	
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Ile Val Ser Lys Gln Lys Leu Glu Leu Lys Thr Thr Glu Ala Gly Pro	
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Arg Met Ile Pro Gly Lys Gln Val Ala Gly Val Ile Lys Ala Val Asp	
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Ser Lys Tyr Lys Ala Ile Pro Ile Val Gly Gln Val Leu Glu Arg Val	
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Cys Lys Gly Cys Pro Ser Leu Ala Glu His Trp Lys Ser Ile Arg Lys	
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aac ctg gag cct gaa aac ctg tcc aag gcc gag gct gtc cag agc ttc	1011
Asn Leu Glu Pro Glu Asn Leu Ser Lys Ala Glu Ala Val Gln Ser Phe	
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Leu Ala Phe Ile Gln His Leu Arg Thr Ser Arg Arg Glu Glu Ile Leu	
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Gln Ile Leu Lys Ala Glu Lys Lys Glu Val Leu Pro Gln Leu Val Asp	
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ctc Leu	tat Tyr 395	gcc Ala	tgt Cys	ggc Gly	ttt Phe 400	gcc Ala	acc Thr	cac His	cct Pro	gat Asp	gaa Glu 405	gaa Glu	ctc Leu	cta Leu	cga Arg	1251
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Ser	Phe	Val	Lys	Ala	Gly	Leu	Glu	Ser	Arg	Ala	Glu	Thr	Glu	Ala	Gly	
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Cys Met Gln Met Asp Lys Ala Glu Ala Pro Leu Arg Gln Phe Glu Thr				
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Lys Tyr Glu Arg Leu Ser Thr Gly Arg Gly Tyr Val Ser Arg Arg Arg				
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Ser Gly Gly Trp Phe				
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